

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: HE, ET AL.
- (ii) TITLE OF INVENTION: Interleukin-1 β Converting Enzyme
Like Apoptosis Protease- 3 and 4
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
CECCHI, STEWART & OLSTEIN
- (B) STREET: 6 BECKER FARM ROAD
- (C) CITY: ROSELAND
- (D) STATE: NEW JERSEY
- (E) COUNTRY: USA
- (F) ZIP: 07068
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 3.5 INCH DISKETTE
- (B) COMPUTER: IBM PS/2
- (C) OPERATING SYSTEM: MS-DOS
- (D) SOFTWARE: WORD PERFECT 5.1
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE: submitted herewith
- (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA
- (A) APPLICATION NUMBER: 08/334,251
- (B) FILING DATE: 11/1/94

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: FERRARO, GREGORY D.
(B) REGISTRATION NUMBER: 36,134
(C) REFERENCE/DOCKET NUMBER: 325800-???

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 201-994-1700
(B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 1371 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCACGAGAAA	CTTTGCTGTG	CGCCTTCTCC	CGCGCGCGGG	CTCAACTTTG	TAGAGCGAGG	60
GGCCAACTTG	GCAGAGCGCG	CGGCCAGCTT	TGCAGAGAGC	GCCCTCCAGG	GACTATGCGT	120
GCGGGGACAC	GGGTCGCTTT	GGGCTCTTCC	ACCCCTGCGG	AGCGCACTAC	CCCAGGCCAG	180
GGGCGGTGCA	AGCCCCGCCC	GGCCCTACCC	AGGGCGGCTC	CTCCCTCCGC	AGCGCCGAGA	240
CTTTTAGTTT	CGCTTTCGCT	AAAGGGGCCC	CAGACCCTTG	CTGCGGAGCG	ACGGAGAGAG	300
ACTGTGCCAG	TCCCAGCCGC	CCTACCGCCG	TGGGAACGAT	GGCAGATGAT	TCAGGGCTGT	360
ATTGAAGAGC	AGGGGGTTGA	GGATTCAGCA	AATGAAGATT	CAGTGGATGC	TAAGCCAGAC	420
CGGTCCTCGT	TTGTACCGTC	CCTCTTCAGT	AAGAAGAAGA	AAAATGTCAC	CATGCGATCC	480
ATCAAGACCA	CCCGGGACCG	AGTGCCTACA	TATCAGTACA	ACATGAATTT	TGAAAAGCTG	540
GGCAAATGCA	TCATAATAAA	CAACAAGAAC	TTTGATAAAG	TGACAGGTAT	GGGCGTTCGA	600
AACGGAACAG	ACAAAGATGC	CGAGGCGCTC	TTCAAGTGCT	TCCGAAGCCT	GGGTTTTGAC	660
GTGATTGTCT	ATAATGACTG	CTCTTGTC	AAGATGCAAG	ATCTGCTTAA	AAAAGCTTCT	720
GAAGAGGACC	ATACAAATGC	CGCCTGCTTC	GCCTGCATCC	TCTTAAGCCA	TGGAGAAGAA	780
AATGTAATTT	ATGGGAAAGA	TGGTGTCA	CCAATAAAGG	ATTTGACAGC	CCACTTTAGG	840
GGGGATAGAT	GCAAAACCCT	TTTAGAGAAA	CCCAAACCTCT	TCTTCATTCA	GGCTTGCCGA	900
GGGACCGAGC	TTGATGATGG	CATCCAGGCC	GACTCGGGGC	CCATCAATGA	CACAGATGCT	960

AATCCTCGAT ACAAGATCCC AGTGAAGCT GACTTCCTCT TCGCCTATTC CACGGTTCCA 1020
 GGCTATTACT CGTGGAGGAG CCCAGGAAGA GGCTCCTGGT TTGTGCAAGC CCTCTGCTCC 1080
 ATCCTGGAGG AGCACGGAAA AGACCTGGAA ATCATGCAAA TCCTCCACCA GGGTGAATGA 1140
 CAGAGTTGCC AGGCACTTTG AGTCTCAGTC TGATGACCCA CACTTCCATG AGAAGAAGCA 1200
 GATCCCCTGT GTGGTCTCCA TGCTCACCAA GGAAGTCTAC TTCAGTCAAT AGCCATATCA 1260
 GGGGTACATT CTAGCTGAGA AGCAATGGGT CACTCATTA TGAATCACAT TTTTATATGC 1320
 TCTTGAAATA TTCAGAAATT CTCCAGGATT TTAATTCAG GAAAATGTAT T 1371

(3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 341 AMINO ACIDS
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS:
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Ala	Gly	Thr	Arg	Val	Ala	Leu	Gly	Ser	Ser	Thr	Pro	Ala	5	10	15
Glu	Arg	Thr	Thr	Pro	Ser	Gln	Gly	Arg	Cys	Lys	Pro	Arg	Pro	Ala	20	25	30
Leu	Pro	Arg	Ala	Ala	Pro	Pro	Ser	Ala	Ala	Pro	Arg	Leu	Leu	Val	35	40	45
Ser	Leu	Ser	Leu	Lys	Gly	Pro	Gln	Thr	Leu	Ala	Ala	Glu	Arg	Arg	50	55	60
Arg	Glu	Thr	Val	Pro	Val	Pro	Ala	Ala	Leu	Pro	Pro	Trp	Glu	Arg	65	70	75
Thr	Gln	Met	Ile	Gln	Gly	Cys	Ile	Glu	Glu	Gln	Gly	Val	Glu	Asp	80	85	90
Ser	Ala	Asn	Glu	Asp	Ser	Val	Asp	Ala	Lys	Pro	Asp	Arg	Ser	Ser	95	100	105
Phe	Val	Pro	Ser	Leu	Phe	Ser	Lys	Lys	Lys	Lys	Asn	Val	Thr	Met	110	115	120
Arg	Ser	Ile	Lys	Thr	Thr	Arg	Asp	Arg	Val	Pro	Thr	Tyr	Gln	Tyr			

				125					130					135
Asn	Met	Asn	Phe	Glu	Lys	Leu	Gly	Lys	Cys	Ile	Ile	Ile	Asn	Asn
				140					145					150
Lys	Asn	Phe	Asp	Lys	Val	Thr	Gly	Met	Gly	Val	Arg	Asn	Gly	Thr
				155					160					165
Asp	Lys	Asp	Ala	Glu	Ala	Leu	Phe	Lys	Cys	Phe	Arg	Ser	Leu	Gly
				170					175					180
Phe	Asp	Val	Ile	Val	Tyr	Asn	Asp	Cys	Ser	Cys	Ala	Lys	Met	Gln
				185					190					195
Asp	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Glu	Asp	His	Thr	Asn	Ala	Ala
				200					205					210
Cys	Phe	Ala	Cys	Ile	Leu	Leu	Ser	His	Gly	Glu	Glu	Asn	Val	Ile
				215					220					225
Tyr	Gly	Lys	Asp	Gly	Val	Thr	Pro	Ile	Lys	Asp	Leu	Thr	Ala	His
				230					235					240
Phe	Arg	Gly	Asp	Arg	Cys	Lys	Thr	Leu	Leu	Glu	Lys	Pro	Lys	Leu
				245					250					255
Phe	Phe	Ile	Gln	Ala	Cys	Arg	Gly	Thr	Glu	Leu	Asp	Asp	Gly	Ile
				260					265					270
Gln	Ala	Asp	Ser	Gly	Pro	Ile	Asn	Asp	Thr	Asp	Ala	Asn	Pro	Arg
				275					280					285
Tyr	Lys	Ile	Pro	Val	Glu	Ala	Asp	Phe	Leu	Phe	Ala	Tyr	Ser	Thr
				290					295					300
Val	Pro	Gly	Tyr	Tyr	Ser	Trp	Arg	Ser	Pro	Gly	Arg	Gly	Ser	Trp
				305					310					315
Phe	Val	Gln	Ala	Leu	Cys	Ser	Ile	Leu	Glu	Glu	His	Gly	Lys	Asp
				320					325					330
Leu	Glu	Ile	Met	Gln	Ile	Leu	His	Gln	Gly	Glu				
				335					340					

(i) SEQUENCE CHARACTERISTICS

-43-

(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCACGAGCGG	ATGGGTGCTA	TTGTGAGGCG	GTTGTAGAAG	AGTTTCGTGA	GTGCTCGCAG	60
CTCATACTTG	TGGCTGTGTA	TCCGTGGCCA	CAGCTGGTTG	GCGTCGCCTT	GAAATCCCAG	120
GCCGTGAGGA	GTTAGCGAGC	CCTGCTCACA	CTCGGCGCTC	TGGTTTTCCG	TGGGTGTGCC	180
CTGCACCTGC	CTCTTCCCGC	ATTCTCATT	ATAAAGGTAT	CCATGGAGAA	CACTGAAAAC	240
TCAGTGGAAT	CAAAATCCAT	TAAAAATTTG	GAACCAAAGA	TCATACATGG	AAGCGAATCA	300
ATGGACTCTG	GAATATCCCT	GGACAACAGT	TATAAAATGG	ATTATCCTGA	GATGGGTTTA	360
TGTATAATAA	TTAATAATAA	GAATTTTCAT	AAAAGCACTG	GAATGACATC	TCGGTCTGGT	420
ACAGATGTCT	ATGCAGCAAA	CCTCAGGGAA	ACATTCAGAA	ACTTGAAATA	TGAAGTCAGG	480
AATAAAAATG	ATCTTACACG	TGAAGAAATT	GTGGAATTGA	TGCGTGATGT	TTCTAAAGAA	540
GATCACAGCA	AAAGGAGCAG	TTTTGTTTGT	GTGCTTCTGA	GCCATGGTGA	AGAAGGAATA	600
ATTTTTGGAA	CAAATGGACC	TGTTGACCTG	AAAAAAATAA	CAAACTTTTT	CAGAGGGGAT	660
CGTTGTAGAA	GTCTAACTGG	AAAACCCAAA	CTTTTCATTA	TTCAGGCCTG	CCGTGGTACA	720
GAAGTGGACT	GTGGCATTGA	GACAGACAGT	GGTGTGTATG	ATGACATGGC	GTGTCATAAA	780
ATACCAGTGG	AGGCCGACTT	CTTGATGCA	TACTCCACAG	CACCTGGTTA	TTATTCTTGG	840
CGAAATTCAA	AGGATGGCTC	CTGGTTCATC	CAGTCGCTTT	GTGCCATGCT	GAAACAGTAT	900
GCCGACAAGC	TTGAATTTAT	GCACATTCTT	ACCCGGGTTA	ACCGAAAGGT	GGCAACAGAA	960
TTTGAGTCCT	TTTCCTTTGA	CGCTACTTTT	CATGCAAAGA	AACAGATTCC	ATGTATTGTT	1020
TCCATGCTCA	CAAAAGAACT	CTATTTTTAT	CACTAAAGAA	ATGGTTGGTT	GGTGGTTTTT	1080
TTTAGTTTGT	ATGCCAAGTG	AGAAGATGGT	ATATTGGGGT	ACTGTATTTT	CCTCTCATTG	1140
GGGACCTACT	CTCATGCTG					1159

(5) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 277 AMINO ACIDS
(B) TYPE: AMINO ACID
(C) STRANDEDNESS:
(D) TOPOLOGY: LINEAR 2

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Glu	Asn	Thr	Glu	Asn	Ser	Val	Asp	Ser	Lys	Ser	Ile	Lys	Asn	5	10	15
Leu	Glu	Pro	Lys	Ile	Ile	His	Gly	Ser	Glu	Ser	Met	Asp	Ser	Gly	20	25	30
Ile	Ser	Leu	Asp	Asn	Ser	Tyr	Lys	Met	Asp	Tyr	Pro	Glu	Met	Gly	35	40	45
Leu	Cys	Ile	Ile	Ile	Asn	Asn	Lys	Asn	Phe	His	Lys	Ser	Thr	Gly	50	55	60
Met	Thr	Ser	Arg	Ser	Gly	Thr	Asp	Val	Asp	Ala	Ala	Asn	Leu	Arg	65	70	75
Glu	Thr	Phe	Arg	Asn	Leu	Lys	Tyr	Glu	Val	Arg	Asn	Lys	Asn	Asp	80	85	90
Leu	Thr	Arg	Glu	Glu	Ile	Val	Glu	Leu	Met	Arg	Asp	Val	Ser	Lys	95	100	105
Glu	Asp	His	Ser	Lys	Arg	Ser	Ser	Phe	Val	Cys	Val	Leu	Leu	Ser	110	115	120
His	Gly	Glu	Glu	Gly	Ile	Ile	Phe	Gly	Thr	Asn	Gly	Pro	Val	Asp	125	130	135
Leu	Lys	Lys	Ile	Thr	Asn	Phe	Phe	Arg	Gly	Asp	Arg	Cys	Arg	Ser	140	145	150
Leu	Thr	Gly	Lys	Pro	Lys	Leu	Phe	Ile	Ile	Gln	Ala	Cys	Arg	Gly	155	160	165
Thr	Glu	Leu	Asp	Cys	Gly	Ile	Glu	Thr	Asp	Ser	Gly	Val	Asp	Asp	170	175	180
Asp	Met	Ala	Cys	His	Lys	Ile	Pro	Val	Glu	Ala	Asp	Phe	Leu	Tyr	185	190	195
Ala	Tyr	Ser	Thr	Ala	Pro	Gly	Tyr	Tyr	Ser	Trp	Arg	Asn	Ser	Lys	200	205	210
Asp	Gly	Ser	Trp	Phe	Ile	Gln	Ser	Leu	Cys	Ala	Met	Leu	Lys	Gln	215	220	225
Tyr	Ala	Asp	Lys	Leu	Glu	Phe	Met	His	Ile	Leu	Thr	Arg	Val	Asn	230	235	240
Arg	Lys	Val	Ala	Thr	Glu	Phe	Glu	Ser	Phe	Ser	Phe	Asp	Ala	Thr			

- (A) LENGTH: 31 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
GATCGGATCC ATGGAGAACA CTGAAACTC A

31

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 31 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
GTACTCTAGA TTAGTGATAA AAATAGAGTT C

31

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 22 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
GACTATGCGT GCGGGGACAC GG

22

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 53 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AATCAAGCGT AGTCTGGGAC GTCGTATGG TATTCACCCT GGTGGAGGAT TTG 53

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 21 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACCATGGAGA ACACTGAAAA C

21

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 53 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
AATCAAGCGT AGTCTGGGAC GTCGTATGGG TAGTGATAAA AATAGAGTTC TTT 53

09513609.074000